



OIEP

## RAW SEQUENCE LISTING

DATE: 04/17/2002

PATENT APPLICATION: US/10/054,435

TIME: 11:43:33

Input Set : N:\Crf3\RULE60\10054435.raw

Output Set: N:\CRF3\04172002\J054435.raw

1 <110> APPLICANT: Bollag, Gideon  
 2 Crompton, Anne  
 3 North, Anne  
 4 Sharma, Sanju  
 5 Roscoe, William  
 6 <120> TITLE OF INVENTION: Methods and Compositions for Treating Abnormal Cell  
 7 Growth Related to Unwanted Guanine Nucleotide Exchange  
 8 Factor Activity  
 9 <130> FILE REFERENCE: 1028-US  
 10 <140> CURRENT APPLICATION NUMBER: 10/054,435  
 11 <141> CURRENT FILING DATE: 2002-01-18  
 13 <150> PRIOR APPLICATION NUMBER: 09/079,812  
 14 <151> PRIOR FILING DATE: 1998-05-15  
 16 <150> PRIOR APPLICATION NUMBER: 60/049,879  
 17 <151> PRIOR FILING DATE: 1997-06-17  
 18 <160> NUMBER OF SEQ ID NOS: 33  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 3171  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Liver Rac GEF  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
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 30 tctggctcta tttcc atg gag acc agg gaa tct gaa gat ttg gaa aag acc 111  
 W--> 31 Met Glu Thr Arg Glu Ser Glu Asp Leu Glu Lys Thr  
 32 1 5 10  
 33 cgg agg aaa tca gca agt gat caa tgg aac act gat aat gaa cca gcc 159  
 34 Arg Arg Lys Ser Ala Ser Asp Gln Trp Asn Thr Asp Asn Glu Pro Ala  
 35 15 20 25  
 36 aag gtg aaa cct gag tta ctc cca gaa aaa gag gag act tct caa gct 207  
 37 Lys Val Lys Pro Glu Leu Leu Pro Glu Lys Glu Glu Thr Ser Gln Ala  
 38 30 35 40  
 39 gac cag gat atc caa gac aaa gag cct cat tgc cac atc cca att aag 255  
 40 Asp Gln Asp Ile Gln Asp Lys Glu Pro His Cys His Ile Pro Ile Lys  
 41 45 50 55 60  
 42 aga aat tcc atc ttc aat cgc tcc ata aga cgc aaa agc aaa gcc aag 303  
 43 Arg Asn Ser Ile Phe Asn Arg Ser Ile Arg Arg Lys Ser Lys Ala Lys  
 44 65 70 75  
 45 gcc aga gac aac ccc gaa cgg aac gcc agc tgc ctg gca gat tca cag 351  
 46 Ala Arg Asp Asn Pro Glu Arg Asn Ala Ser Cys Leu Ala Asp Ser Gln

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47		80		85		90		
48	gac	aat	gga	aaa	tct	gta	aat	gag
49	Asp	Asn	Gly	Lys	Ser	Val	Asn	Glu
50			95				100	
51	agc	aga	atg	cct	cct	tgc	aga	aca
52	Ser	Arg	Met	Pro	Pro	Cys	Arg	Thr
53			110				115	
54	cag	gaa	atg	agt	gag	tcg	tcc	tcc
55	Gln	Glu	Met	Ser	Glu	Ser	Ser	Thr
56			125				130	
57	gag	gag	tgg	ccg	gcc	ctg	gcc	gac
58	Glu	Glu	Trp	Pro	Ala	Leu	Ala	Asp
59					145			150
60	ctg	cgg	atg	atc	cac	ccc	att	ccc
61	Leu	Arg	Met	Ile	His	Pro	Ile	Pro
62					160			165
63	gaa	caa	ata	ggg	ctc	ctg	tat	cag
64	Glu	Gln	Ile	Gly	Leu	Leu	Tyr	Gln
65					175			180
66	caa	gaa	atc	gaa	acc	agg	agg	caa
67	Gln	Glu	Ile	Glu	Thr	Arg	Arg	Gln
68					190			195
69	acc	aat	ggg	tcc	ccg	gcc	agt	gag
70	Thr	Asn	Gly	Ser	Pro	Ala	Ser	Glu
71						205		210
72	gag	gag	gag	gag	gag	gag	ccg	gcc
73	Glu	Glu	Glu	Glu	Glu	Glu	Pro	Ala
74						225		230
75	ccc	cag	atc	tgc	ctg	ctc	agt	aac
76	Pro	Gln	Ile	Cys	Leu	Leu	Ser	Asn
77						240		245
78	cag	gat	ctt	ccc	gag	atc	cgg	agc
79	Gln	Asp	Leu	Pro	Glu	Ile	Arg	Ser
80						255		260
81	cct	gag	gag	att	aag	ctg	cag	gag
82	Pro	Glu	Glu	Ile	Lys	Leu	Gln	Glu
83						270		275
84	gag	gcg	tcc	tac	tac	aag	agt	ctg
85	Glu	Ala	Ser	Tyr	Tyr	Lys	Ser	Leu
86						285		290
87	gag	aac	gag	cgg	ata	agg	aag	atc
88	Glu	Asn	Glu	Arg	Ile	Arg	Lys	Ile
89						305		310
90	ctc	ttc	tcc	aac	gtc	ctg	gac	gtg
91	Leu	Phe	Ser	Asn	Val	Leu	Asp	Val
92						320		325
93	ctg	gag	ctg	gag	cac	cgg	atg	gag
94	Leu	Glu	Leu	Glu	His	Arg	Met	Glu
95						335		340

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96   tgt gac atc gtg tac cgt tat gcg gcc gac cac ttc tct gtc tac atc   1167
97   Cys Asp Ile Val Tyr Arg Tyr Ala Ala Asp His Phe Ser Val Tyr Ile
98       350                      355                      360
99   acc tac gtc agc aat cag acc tac cag gag cgg acc tat aag cag ctg   1215
100   Thr Tyr Val Ser Asn Gln Thr Tyr Gln Glu Arg Thr Tyr Lys Gln Leu
101   365                      370                      375                      380
102   ctc cag gag aag gca gct ttc cgg gag ctg atc gcg cag cta gag ctc   1263
103   Leu Gln Glu Lys Ala Ala Phe Arg Glu Leu Ile Ala Gln Leu Glu Leu
104       385                      390                      395
105   gac ccc aag tgc agg ggg ctg ccc ttc tcc ttc ctc atc ctg cct   1311
106   Asp Pro Lys Cys Arg Gly Leu Pro Phe Ser Ser Phe Leu Ile Leu Pro
107       400                      405                      410
108   ttc cag agg atc aca cgc ctc aag ctg ttg gtc cag aac atc ctg aag   1359
109   Phe Gln Arg Ile Thr Arg Leu Lys Leu Leu Val Gln Asn Ile Leu Lys
110       415                      420                      425
111   agg gta gaa gag agg tct gag cgg gag tgc act gct ttg gat gct cac   1407
112   Arg Val Glu Glu Arg Ser Glu Arg Glu Cys Thr Ala Leu Asp Ala His
113       430                      435                      440
114   aag gag ctg gaa atg gtg gtg aag gca tgc aac gag ggc gtc agg aaa   1455
115   Lys Glu Leu Glu Met Val Val Lys Ala Cys Asn Glu Gly Val Arg Lys
116   445                      450                      455                      460
117   atg agc cgc acg gaa cag atg atc agc att cag aag aag atg gag ttc   1503
118   Met Ser Arg Thr Glu Gln Met Ile Ser Ile Gln Lys Lys Met Glu Phe
119       465                      470                      475
120   aag atc aag tcg gtg ccc atc atc tcc cac tcc cgc tgg ctg ctg aag   1551
121   Lys Ile Lys Ser Val Pro Ile Ile Ser His Ser Arg Trp Leu Leu Lys
122       480                      485                      490
123   cag ggt gag ctg cag cag atg tca ggc ccc aag acc tcc cgg acc ctg   1599
124   Gln Gly Glu Leu Gln Gln Met Ser Gly Pro Lys Thr Ser Arg Thr Leu
125       495                      500                      505
126   agg acc aag aag ctc ttc cac gaa att tac ctc ttc ctg ttc aac gac   1647
127   Arg Thr Lys Lys Leu Phe His Glu Ile Tyr Leu Phe Leu Phe Asn Asp
128       510                      515                      520
129   ctg ctg gtg atc tgc cgg cag att cca gga gac aag tac cag gta ttt   1695
130   Leu Leu Val Ile Cys Arg Gln Ile Pro Gly Asp Lys Tyr Gln Val Phe
131   525                      530                      535                      540
132   gac tca gct ccg cgg gga ctg ctg cgt gtg gag gag ctg gag gac cag   1743
133   Asp Ser Ala Pro Arg Gly Leu Leu Arg Val Glu Glu Leu Glu Asp Gln
134       545                      550                      555
135   ggc cag acg ctg gcc aac gtg ttc atc ctg cgg ctg ctg gag aac gca   1791
136   Gly Gln Thr Leu Ala Asn Val Phe Ile Leu Arg Leu Leu Glu Asn Ala
137       560                      565                      570
138   gat gac cgg gag gcc acc tac atg cta aag gcg tcc tct cag agt gag   1839
139   Asp Asp Arg Glu Ala Thr Tyr Met Leu Lys Ala Ser Ser Gln Ser Glu
140       575                      580                      585
141   atg aag cgt tgg atg acc tca ctg gcc ccc aac agg agg acc aag ttt   1887
142   Met Lys Arg Trp Met Thr Ser Leu Ala Pro Asn Arg Arg Thr Lys Phe
143       590                      595                      600
144   gtt tcg ttc aca tcc cgg ctg ctg gac tgc ccc cag gtc cag tgc gtg   1935

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145 Val Ser Phe Thr Ser Arg Leu Leu Asp Cys Pro Gln Val Gln Cys Val
146 605 610 615 620
147 cac cca tac gtg gct cag cag cca gac gag ctg acg ctg gag ctc gcc 1983
148 His Pro Tyr Val Ala Gln Gln Pro Asp Glu Leu Thr Leu Glu Leu Ala
149 625 630 635
150 gag atc ctc aac atc ctg gac aag act gag gac ggg tgg atc ttt ggc 2031
151 Asp Ile Leu Asn Ile Leu Asp Lys Thr Asp Asp Gly Trp Ile Phe Gly
152 640 645 650
153 gag cgt ctg cac gac cag gag aga ggc tgg ttc ccc agc tcc atg act 2079
154 Glu Arg Leu His Asp Gln Glu Arg Gly Trp Phe Pro Ser Ser Met Thr
155 655 660 665
156 gag gag atc ttg aat ccc aag atc cgg tcc cag aac ctc aag gaa tgt 2127
157 Glu Glu Ile Leu Asn Pro Lys Ile Arg Ser Gln Asn Leu Lys Glu Cys
158 670 675 680
159 ttc cgt gtc cac aag atg gat gac cct cag cgc agc cag aac aag gac 2175
160 Phe Arg Val His Lys Met Asp Asp Pro Gln Arg Ser Gln Asn Lys Asp
161 685 690 695 700
162 cgc agg aag ctg ggc agc cgg aat cgg caa tga ccccccaccca gggggccagc 2228
163 Arg Arg Lys Leu Gly Ser Arg Asn Arg Gln
164 705 710
165 gggagcaggg cctgcatgag accccgacag aaggtggggg gggggggggg ggctctggga 2288
166 agcacaggcc agcacctccc caggtggcag gatctggcct ggggtgcccg gccctcatcc 2348
167 ctgcccacgc agtgagtgtc catgtgtctt ggccccttgc tcgcaaactg gataaaaggg 2408
168 gcccaagcct ctctgatgc atttgtaaac aagaaggttt cagcagtatt acaccacctc 2468
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176 cccaggtgtt ttaaggaatg aattggtcac tgcacttgtt atcgattatg gttctgagaa 2948
177 aagcaaatat cggaattcct gcagcccggg aaatggggcc acgcccaggg agtggccggc 3008
178 cctggccgac agccccacca cgctcaccga ggccctgcgg atgatccacc ccattcccgc 3068
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180 atcgactctc caaaaaaaaa aaaaaaaaaa gatctttaat taa 3171
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183 <211> LENGTH: 710
184 <212> TYPE: PRT
185 <213> ORGANISM: Liver Rac GEF
186 <400> SEQUENCE: 2
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190 20 25 30
191 Glu Leu Leu Pro Glu Lys Glu Glu Thr Ser Gln Ala Asp Gln Asp Ile
192 35 40 45
193 Gln Asp Lys Glu Pro His Cys His Ile Pro Ile Lys Arg Asn Ser Ile
194 50 55 60

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195   Phe Asn Arg Ser Ile Arg Arg Lys Ser Lys Ala Lys Ala Arg Asp Asn
196      65                      70                      75                      80
197   Pro Glu Arg Asn Ala Ser Cys Leu Ala Asp Ser Gln Asp Asn Gly Lys
198                      85                      90                      95
199   Ser Val Asn Glu Pro Leu Thr Leu Asn Ile Pro Trp Ser Arg Met Pro
200                      100                      105                      110
201   Pro Cys Arg Thr Ala Met Gln Thr Asp Pro Gly Ala Gln Glu Met Ser
202                      115                      120                      125
203   Glu Ser Ser Ser Thr Pro Gly Asn Gly Ala Thr Pro Glu Glu Trp Pro
204                      130                      135                      140
205   Ala Leu Ala Asp Ser Pro Thr Thr Leu Thr Glu Ala Leu Arg Met Ile
206                      145                      150                      155                      160
207   His Pro Ile Pro Ala Asp Ser Trp Arg Asn Leu Ile Glu Gln Ile Gly
208                      165                      170                      175
209   Leu Leu Tyr Gln Glu Tyr Arg Asp Lys Ser Thr Leu Gln Glu Ile Glu
210                      180                      185                      190
211   Thr Arg Arg Gln Gln Asp Ala Glu Ile Glu Asp Asn Thr Asn Gly Ser
212                      195                      200                      205
213   Pro Ala Ser Glu Asp Thr Pro Glu Glu Glu Glu Glu Glu Glu Glu
214                      210                      215                      220
215   Glu Glu Pro Ala Ser Pro Pro Glu Arg Lys Thr Leu Pro Gln Ile Cys
216                      225                      230                      235                      240
217   Leu Leu Ser Asn Pro His Ser Arg Phe Asn Leu Trp Gln Asp Leu Pro
218                      245                      250                      255
219   Glu Ile Arg Ser Ser Gly Val Leu Glu Ile Leu Gln Pro Glu Glu Ile
220                      260                      265                      270
221   Lys Leu Gln Glu Ala Met Phe Glu Leu Val Thr Ser Glu Ala Ser Tyr
222                      275                      280                      285
223   Tyr Lys Ser Leu Asn Leu Leu Val Ser His Phe Met Glu Asn Glu Arg
224                      290                      295                      300
225   Ile Arg Lys Ile Leu His Pro Ser Glu Ala His Ile Leu Phe Ser Asn
226                      305                      310                      315                      320
227   Val Leu Asp Val Leu Ala Val Ser Glu Arg Phe Leu Leu Glu Leu Glu
228                      325                      330                      335
229   His Arg Met Glu Glu Asn Ile Val Ile Ser Asp Val Cys Asp Ile Val
230                      340                      345                      350
231   Tyr Arg Tyr Ala Ala Asp His Phe Ser Val Tyr Ile Thr Tyr Val Ser
232                      355                      360                      365
233   Asn Gln Thr Tyr Gln Glu Arg Thr Tyr Lys Gln Leu Leu Gln Glu Lys
234                      370                      375                      380
235   Ala Ala Phe Arg Glu Leu Ile Ala Gln Leu Glu Leu Asp Pro Lys Cys
236                      385                      390                      395                      400
237   Arg Gly Leu Pro Phe Ser Ser Phe Leu Ile Leu Pro Phe Gln Arg Ile
238                      405                      410                      415
239   Thr Arg Leu Lys Leu Leu Val Gln Asn Ile Leu Lys Arg Val Glu Glu
240                      420                      425                      430
241   Arg Ser Glu Arg Glu Cys Thr Ala Leu Asp Ala His Lys Glu Leu Glu
242                      435                      440                      445
243   Met Val Val Lys Ala Cys Asn Glu Gly Val Arg Lys Met Ser Arg Thr

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## VERIFICATION SUMMARY

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L:31 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 1, CDS LOCATION:0..76

L:474 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:30, CDS LOCATION: Complement (1)..(198)